

WEST Search History

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DATE: Wednesday, June 29, 2005

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L12	\$tgaaatgctc a\$	0
<input type="checkbox"/>	L11	L9 and L2	10
<input type="checkbox"/>	L10	L9 and L1	0
<input type="checkbox"/>	L9	tgaaatgctc	12
<input type="checkbox"/>	L8	tgaaatgctc a	0
<input type="checkbox"/>	L7	tgaaatgctca	0
<input type="checkbox"/>	L6	tgaatgctca	5
<input type="checkbox"/>	L5	L4 and L2	52
<input type="checkbox"/>	L4	CYP3\$	805
<input type="checkbox"/>	L3	L2 and L1	1
<input type="checkbox"/>	L2	(536/23.1 536/24.3 536/24.31 536/24.33)! [CCLS]	15186
<input type="checkbox"/>	L1	(wojnowski or eiselt).in.	65

END OF SEARCH HISTORY

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 16:05:53 ; Search time 63.5 Seconds
(without alignments)
133.996 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 18
Sequence: 1 tgaaatgctca 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1000%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool h/US10070587/runat_27052005_162824_
26715/app_query.fasta_1.199
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=1000 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070587 @CGN_1_1_101 @runat_27052005_162824_26715 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				DB	ID	Description
	No.	Score	Match	Length			
c	1	19	100.0	8	3	AAB11860	Aab11860 [Nle4, D-
c	2	19	100.0	8	3	AAB11856	Aab11856 Alpha-MSH
c	3	19	100.0	8	3	AAB11861	Aab11861 [Nle4, D-
c	4	19	100.0	8	3	AAB11854	Aab11854 Alpha-MSH
c	5	19	100.0	8	3	AAB11855	Aab11855 Alpha-MSH
c	6	19	100.0	8	4	AAB90830	Aab90830 Adrenocor
c	7	19	100.0	8	4	ABB50731	Abb50731 Human sec
c	8	19	100.0	8	5	ABG69448	Abg69448 Vascular
c	9	19	100.0	8	6	ABO44988	Abo44988 Novel hum
c	10	19	100.0	8	7	ABO26468	Abo26468 Protein a
c	11	19	100.0	8	7	ADB81284	Adb81284 Biologica
c	12	19	100.0	8	7	AAE39604	Aae39604 Peptide #
c	13	19	100.0	8	7	ADE01189	Ade01189 Bovine Se
c	14	19	100.0	8	7	AAO27599	Aao27599 Bovine BS
c	15	19	100.0	8	7	AAO27581	Aao27581 Bovine BS
c	16	19	100.0	8	8	ADF90482	Adf90482 Human Fas
c	17	19	100.0	8	8	ADR28520	Adr28520 Human her
c	18	19	100.0	9	2	AAR21469	Aar21469 Sequence
c	19	19	100.0	9	2	AAR37043	Aar37043 Peptide c
c	20	19	100.0	9	2	AAY02419	Aay02419 Somatosta
c	21	19	100.0	9	2	AAY41913	Aay41913 Rheumatoi
c	22	19	100.0	9	2	AAY41845	Aay41845 Rheumatoi
c	23	19	100.0	9	2	AAY41844	Aay41844 Rheumatoi
c	24	19	100.0	9	2	AAY01001	Aay01001 Bacterial
c	25	19	100.0	9	3	AAY62834	Aay62834 PB-cadher
c	26	19	100.0	9	4	AAB83896	Aab83896 Amino aci
c	27	19	100.0	9	4	AAM22284	Aam22284 HIV pepti
c	28	19	100.0	9	4	AAG88964	Aag88964 HER2/neu
c	29	19	100.0	9	4	AAB46153	Aab46153 HCMV type
c	30	19	100.0	9	4	AAB46154	Aab46154 HCMV type
c	31	19	100.0	9	6	ABJ19537	Abj19537 CODEHOP g
c	32	19	100.0	9	6	ABJ19492	Abj19492 CODEHOP g
c	33	19	100.0	9	6	ABJ20028	Abj20028 MHC bindi
c	34	19	100.0	9	7	ADD98446	Add98446 Human 193
c	35	19	100.0	9	7	ADD99604	Add99604 Human 193
c	36	19	100.0	9	7	ADD99729	Add99729 Human 193
c	37	19	100.0	9	7	ADD99023	Add99023 Human 193
c	38	19	100.0	9	7	ADD99350	Add99350 Human 193
c	39	19	100.0	9	7	ADD99904	Add99904 Human 193
c	40	19	100.0	9	7	ADD97046	Add97046 Human 193
c	41	19	100.0	9	7	ADD99028	Add99028 Human 193
c	42	19	100.0	9	7	ADD99360	Add99360 Human 193
c	43	19	100.0	9	7	ADD99518	Add99518 Human 193
c	44	19	100.0	9	7	ADD97609	Add97609 Human 193
c	45	19	100.0	9	7	ADD98212	Add98212 Human 193

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 16:05:52 ; Search time 19.5 Seconds
(without alignments)
84.219 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 18
Sequence: 1 tgaaatgctca 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1000%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10070587/runat_27052005_162826_
26746/app_query.fasta_1.199
-DB=Issued Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=1000 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070587 @CGN_1_1_22 @runat_27052005_162826_26746 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution..

SUMMARIES

Result		Score		Query		DB	ID	Description
No.			Match	Length				
c	1	19	100.0	8	4	US-09-205-258-683		Sequence 683, App
c	2	19	100.0	9	1	US-07-766-682A-2		Sequence 2, Appli
c	3	19	100.0	9	3	US-09-187-859-2390		Sequence 2390, Ap
c	4	19	100.0	9	4	US-09-144-280-5		Sequence 5, Appli
c	5	19	100.0	9	4	US-09-839-542B-2390		Sequence 2390, Ap
c	6	19	100.0	10	1	US-07-766-682A-1		Sequence 1, Appli
c	7	19	100.0	10	1	US-08-671-525B-16		Sequence 16, Appl
c	8	19	100.0	10	1	US-08-671-525B-19		Sequence 19, Appl
c	9	19	100.0	10	1	US-08-672-109B-16		Sequence 16, Appl
c	10	19	100.0	10	1	US-08-672-109B-19		Sequence 19, Appl
c	11	19	100.0	10	2	US-08-842-045-16		Sequence 16, Appl
c	12	19	100.0	10	2	US-08-842-045-19		Sequence 19, Appl
c	13	19	100.0	10	2	US-08-842-238-16		Sequence 16, Appl
c	14	19	100.0	10	2	US-08-842-238-19		Sequence 19, Appl
c	15	19	100.0	10	3	US-08-629-335B-16		Sequence 16, Appl
c	16	19	100.0	10	3	US-08-629-335B-19		Sequence 19, Appl
c	17	19	100.0	10	3	US-09-187-859-2391		Sequence 2391, Ap
c	18	19	100.0	10	4	US-09-839-542B-2391		Sequence 2391, Ap
c	19	19	100.0	11	3	US-09-187-859-2392		Sequence 2392, Ap
c	20	19	100.0	11	4	US-09-205-258-680		Sequence 680, App
c	21	19	100.0	11	4	US-09-839-542B-2392		Sequence 2392, Ap
c	22	19	100.0	11	4	US-10-053-485-21		Sequence 21, Appl
c	23	19	100.0	11	4	US-09-780-070-22		Sequence 22, Appl
c	24	19	100.0	12	1	US-08-129-607-4		Sequence 4, Appli
c	25	19	100.0	12	1	US-08-665-966-1		Sequence 1, Appli
c	26	19	100.0	12	3	US-09-041-780-1		Sequence 1, Appli
c	27	19	100.0	12	4	US-09-216-430C-27		Sequence 27, Appl
c	28	19	100.0	12	5	PCT-US94-00190-4		Sequence 4, Appli
c	29	19	100.0	13	1	US-07-714-167E-6		Sequence 6, Appli
c	30	19	100.0	13	1	US-07-714-167E-7		Sequence 7, Appli
c	31	19	100.0	13	1	US-08-288-681A-7		Sequence 7, Appli
c	32	19	100.0	13	1	US-07-776-272-10		Sequence 10, Appl
c	33	19	100.0	13	1	US-08-349-902B-1		Sequence 1, Appli
c	34	19	100.0	13	1	US-08-349-902B-31		Sequence 31, Appl
c	35	19	100.0	13	1	US-08-349-902B-32		Sequence 32, Appl
c	36	19	100.0	13	1	US-08-671-525B-18		Sequence 18, Appl
c	37	19	100.0	13	1	US-08-672-109B-18		Sequence 18, Appl
c	38	19	100.0	13	1	US-08-741-678-7		Sequence 7, Appli
c	39	19	100.0	13	2	US-08-842-045-18		Sequence 18, Appl
c	40	19	100.0	13	2	US-08-796-598-18		Sequence 18, Appl
c	41	19	100.0	13	2	US-08-447-175A-18		Sequence 18, Appl
c	42	19	100.0	13	2	US-08-842-238-18		Sequence 18, Appl
c	43	19	100.0	13	2	US-08-570-813-1		Sequence 1, Appli
c	44	19	100.0	13	2	US-08-562-983A-1		Sequence 1, Appli
c	45	19	100.0	13	2	US-08-562-983A-4		Sequence 4, Appli

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 16:07:35 ; Search time 257.5 Seconds
(without alignments)
29.473 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 18
Sequence: 1 tgaaatgctca 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 2924198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1000%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10070587/runat_27052005_162829_26819/app_query.fasta_1.199
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR MAX=1000
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10070587 @CGN_1_1_86 @runat_27052005_162829_26819
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8							
Result	Query								
No.	Score	Match	Length	DB	ID	Description			
c 1	19	100.0	8	10	US-09-933-767-683	Sequence 683, App			
c 2	19	100.0	8	14	US-10-033-741-69	Sequence 69, Appl			
c 3	19	100.0	8	14	US-10-004-860-683	Sequence 683, App			
c 4	19	100.0	8	14	US-10-023-282-683	Sequence 683, App			
c 5	19	100.0	8	14	US-10-080-263C-30	Sequence 30, Appl			
c 6	19	100.0	8	16	US-10-445-399-5	Sequence 5, Appli			
c 7	19	100.0	9	10	US-09-865-548A-193	Sequence 193, App			
c 8	19	100.0	9	14	US-10-006-869-2390	Sequence 2390, Ap			
c 9	19	100.0	9	14	US-10-301-644-5	Sequence 5, Appli			
c 10	19	100.0	9	15	US-10-013-312-23	Sequence 23, Appl			
c 11	19	100.0	9	15	US-10-013-312-41	Sequence 41, Appl			
c 12	19	100.0	9	15	US-10-013-312-232	Sequence 232, App			
c 13	19	100.0	9	15	US-10-013-312-235	Sequence 235, App			
c 14	19	100.0	9	15	US-10-013-312-342	Sequence 342, App			
c 15	19	100.0	9	15	US-10-013-312-447	Sequence 447, App			
c 16	19	100.0	9	15	US-10-013-312-512	Sequence 512, App			
c 17	19	100.0	9	15	US-10-013-312-602	Sequence 602, App			
c 18	19	100.0	9	15	US-10-013-312-1404	Sequence 1404, Ap			
c 19	19	100.0	9	15	US-10-013-312-1458	Sequence 1458, Ap			
c 20	19	100.0	9	15	US-10-013-312-1464	Sequence 1464, Ap			
c 21	19	100.0	9	15	US-10-013-312-1473	Sequence 1473, Ap			
c 22	19	100.0	9	15	US-10-013-312-1553	Sequence 1553, Ap			
c 23	19	100.0	9	15	US-10-013-312-1554	Sequence 1554, Ap			
c 24	19	100.0	9	15	US-10-013-312-1612	Sequence 1612, Ap			
c 25	19	100.0	9	15	US-10-013-312-1672	Sequence 1672, Ap			
c 26	19	100.0	9	15	US-10-013-312-1707	Sequence 1707, Ap			
c 27	19	100.0	9	15	US-10-013-312-1745	Sequence 1745, Ap			
c 28	19	100.0	9	15	US-10-013-312-1770	Sequence 1770, Ap			
c 29	19	100.0	9	15	US-10-013-312-1827	Sequence 1827, Ap			
c 30	19	100.0	9	15	US-10-013-312-1889	Sequence 1889, Ap			
c 31	19	100.0	9	15	US-10-013-312-1976	Sequence 1976, Ap			
c 32	19	100.0	9	15	US-10-395-032-2390	Sequence 2390, Ap			
c 33	19	100.0	9	15	US-10-149-138-4313	Sequence 4313, Ap			
c 34	19	100.0	9	15	US-10-182-252A-169	Sequence 169, App			
c 35	19	100.0	9	16	US-10-149-138-4313	Sequence 4313, Ap			
c 36	19	100.0	9	16	US-10-611-440-65	Sequence 65, Appl			
c 37	19	100.0	9	16	US-10-611-440-137	Sequence 137, App			
c 38	19	100.0	9	16	US-10-611-440-138	Sequence 138, App			
c 39	19	100.0	9	16	US-10-611-440-139	Sequence 139, App			
c 40	19	100.0	9	16	US-10-611-440-140	Sequence 140, App			

c	41	19	100.0	9	17	US-10-705-459-193	Sequence 193, App
c	42	19	100.0	10	9	US-09-828-272A-2	Sequence 2, Appli
c	43	19	100.0	10	14	US-10-014-340-34	Sequence 34, Appl
c	44	19	100.0	10	14	US-10-014-340-215	Sequence 215, App
c	45	19	100.0	10	14	US-10-006-869-2391	Sequence 2391, Ap

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 16:05:53 ; Search time 16.5 Seconds
(without alignments)
128.289 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 18
Sequence: 1 tgaaatgctca 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1000%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO spool h/US10070587/runat_27052005_162825_
26731/app_query.fasta_1.199
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=1000 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070587 @CGN_1_1_25 @runat_27052005_162825_26731 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
c 1	19	100.0	13	1	MTCMAD		melanotropin alpha
c 2	19	100.0	13	1	MTHOAD		melanotropin alpha
c 3	19	100.0	18	1	MTHOB		melanotropin beta
c 4	19	100.0	18	2	S27141		hypothetical prote
c 5	19	100.0	24	2	S29749		serum albumin - do
c 6	19	100.0	25	2	D41575		bombinin-like pept
c 7	19	100.0	25	2	A39319		fructokinase (EC 2
c 8	19	100.0	27	2	B41575		bombinin-like pept
c 9	19	100.0	30	2	I39799		CAT-66 - Bacillus
c 10	19	100.0	35	2	C84398		hypothetical prote
c 11	19	100.0	36	2	C59093		hypothetical prote
c 12	19	100.0	37	2	AH0637		conserved hypothet
c 13	19	100.0	39	1	CTDFAS		corticotropin - sp
c 14	19	100.0	39	2	A61127		adrenocorticotropi
c 15	19	100.0	39	2	PN0127		corticotropin - se
c 16	19	100.0	39	2	A01458		corticotropin - fi
c 17	19	100.0	39	2	A01457		corticotropin - ra
c 18	19	100.0	39	2	A01459		corticotropin - os
c 19	19	100.0	39	2	B95022		hypothetical prote
c 20	19	100.0	40	2	B54195		Na+/K+-exchanging
c 21	19	100.0	45	2	S04183		fixB protein - Bra
c 22	19	100.0	46	2	JT0747		epiregulin - rat
c 23	19	100.0	48	2	A86774		hypothetical prote
c 24	19	100.0	48	2	A70206		hypothetical prote
c 25	19	100.0	51	2	S55449		GAM1 protein - Pla
c 26	19	100.0	51	2	AC1789		hypothetical prote
c 27	19	100.0	51	2	AD1413		hypothetical prote
c 28	19	100.0	53	2	JQ1664		hypothetical 6.2K
c 29	19	100.0	53	2	C83180		hypothetical prote
c 30	19	100.0	54	2	B60515		hemoglobin beta ch
c 31	19	100.0	54	2	S66220		defensin AFP1 - He
c 32	19	100.0	55	2	H81732		hypothetical prote
c 33	19	100.0	56	2	A85956		hypothetical prote
c 34	19	100.0	56	2	H89878		conserved hypothet
c 35	19	100.0	57	2	A25159		sinR antagonist si
c 36	19	100.0	57	2	S55452		GAM1 protein - Pla
c 37	19	100.0	58	2	S73144		hypothetical prote
c 38	19	100.0	59	2	D70252		hypothetical prote
c 39	19	100.0	59	2	T34898		hypothetical prote
c 40	19	100.0	60	2	C29606		hypothetical prote
c 41	19	100.0	61	2	T45363		ribosomal protein
c 42	19	100.0	62	2	T00188		hypothetical prote
c 43	19	100.0	63	2	G69941		hypothetical prote
c 44	19	100.0	64	2	D72365		hypothetical prote
c 45	19	100.0	65	2	S77045		transposase ssl127

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 16:05:53 ; Search time 39.5 Seconds
(without alignments)
285.209 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 18
Sequence: 1 tgaaatgctca 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1000%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10070587/runat_27052005_162825_
26721/app_query.fasta_1.199
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=1000 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070587 @CGN_1_1_101 @runat_27052005_162825_26721 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

c	1	19	100.0	13	1	MLA_ANOCA	P41589	anolis caro
c	2	19	100.0	13	1	MLA_CAMDR	P61281	camelus dro
c	3	19	100.0	13	1	MLA_HORSE	P61280	equus cabal
c	4	19	100.0	17	2	Q7RDP8	Q7rdp8	plasmodium
c	5	19	100.0	18	1	MLB_HORSE	P01202	equus cabal
c	6	19	100.0	20	2	Q9TQZ6	Q9tqz6	macaca fasc
c	7	19	100.0	20	2	Q9QV29	Q9qv29	rattus sp.
c	8	19	100.0	21	1	MU11_LITGE	P82066	litoria gen
c	9	19	100.0	23	1	MU12_LITGE	P82067	litoria gen
c	10	19	100.0	23	2	Q8R044	Q8r044	mus musculus
c	11	19	100.0	25	1	BLP4_BOMOR	P29005	bombina ori
c	12	19	100.0	25	1	SCRK_LACLA	Q09124	lactococcus
c	13	19	100.0	26	2	Q9JFP1	Q9jfp1	human t-lym
c	14	19	100.0	27	1	BLP2_BOMOR	P29003	bombina ori
c	15	19	100.0	28	2	Q67745	Q67745	human adeno
c	16	19	100.0	28	2	Q67746	Q67746	human adeno
c	17	19	100.0	29	2	Q69YY8	Q69yy8	homo sapien
c	18	19	100.0	29	2	O13043	O13043	scyliorhinu
c	19	19	100.0	30	2	Q45356	Q45356	bacillus pu
c	20	19	100.0	30	2	Q98NK7	Q98nk7	rhizobium l
c	21	19	100.0	30	2	Q8FYJ0	Q8fyj0	brucella su
c	22	19	100.0	30	2	Q8G035	Q8g035	brucella su
c	23	19	100.0	31	1	ER29_BOVIN	P81623	bos taurus
c	24	19	100.0	31	2	Q6BW72	Q6bw72	debaryomyce
c	25	19	100.0	31	2	Q6LCB7	Q6lcb7	homo sapien
c	26	19	100.0	31	2	Q81SF6	Q81sf6	bacillus an
c	27	19	100.0	33	2	Q9T2M5	Q9t2m5	nicotiana t
c	28	19	100.0	33	2	Q65VR4	Q65vr4	mannheimia
c	29	19	100.0	35	2	Q9HMM0	Q9hmm0	halobacteri
c	30	19	100.0	35	2	Q87GR8	Q87gr8	vibrio para
c	31	19	100.0	36	2	Q7CMJ5	Q7cmj5	bacillus an
c	32	19	100.0	36	2	Q9X2Z0	Q9x2z0	bacillus an
c	33	19	100.0	37	2	Q8XEV1	Q8xev1	salmonella
c	34	19	100.0	37	2	Q734T4	Q734t4	bacillus ce
c	35	19	100.0	37	2	Q7CQR4	Q7cqr4	salmonella
c	36	19	100.0	39	1	COLI_BALBO	P68000	balaenopter
c	37	19	100.0	39	1	COLI_BALPH	P68001	balaenopter
c	38	19	100.0	39	1	COLI_RABIT	P06297	oryctolagus
c	39	19	100.0	39	1	COLI_SQUAC	P01197	squalus aca
c	40	19	100.0	39	1	COLI_STRCA	P01196	struthio ca
c	41	19	100.0	39	2	Q7PGA8	Q7pga8	anopheles g
c	42	19	100.0	39	2	Q97SX3	Q97sx3	streptococc
c	43	19	100.0	39	2	Q8FZB2	Q8fzb2	brucella su
c	44	19	100.0	39	2	Q9YM99	Q9ym99	human immun
c	45	19	100.0	40	2	Q8U4K1	Q8u4k1	pyrococcus

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 22:07:47 ; Search time 1659 Seconds
(without alignments)
321.282 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 11
Sequence: 1 tgaaatgctca 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	11	100.0	11	6	AX098783	AX098783 Sequence
c	2	11	100.0	11	6	AX098784	AX098784 Sequence

c	3	11	100.0	20	6	AR240990	AR240990 Sequence
c	4	11	100.0	24	6	AX445954	AX445954 Sequence
c	5	11	100.0	34	6	AX183751	AX183751 Sequence
c	6	11	100.0	60	6	CQ540175	CQ540175 Sequence
	7	11	100.0	60	6	CQ548821	CQ548821 Sequence
c	8	11	100.0	60	6	CQ550758	CQ550758 Sequence
c	9	11	100.0	63	6	AR521465	AR521465 Sequence
c	10	11	100.0	90	8	ATH521327	AJ521327 Arabidops
	11	11	100.0	100	6	AX988556	AX988556 Sequence
	12	11	100.0	100	6	AX988557	AX988557 Sequence
	13	11	100.0	100	6	AX988558	AX988558 Sequence
	14	11	100.0	104	6	AX645464	AX645464 Sequence
	15	11	100.0	104	6	AX676625	AX676625 Sequence
	16	11	100.0	111	9	AF078528	AF078528 Homo sapi
c	17	11	100.0	117	9	AY516333	AY516333 Homo sapi
c	18	11	100.0	129	8	AY077965	AY077965 Phyllospa
c	19	11	100.0	143	8	AY302062	AY302062 Populus t
	20	11	100.0	146	6	AX795101	AX795101 Sequence
	21	11	100.0	146	8	AY034313	AY034313 Lemna gib
	22	11	100.0	153	6	AX901310	AX901310 Sequence
	23	11	100.0	153	6	BD036843	BD036843 Sequence
	24	11	100.0	154	6	CQ702074	CQ702074 Sequence
c	25	11	100.0	154	8	STSSSPROT	X90943 S.tuberosum
c	26	11	100.0	158	10	F200305S08	AF200312 Mus muscu
	27	11	100.0	159	8	AF393978	AF393978 Pinus tae
	28	11	100.0	165	6	CQ670603	CQ670603 Sequence
	29	11	100.0	166	8	AY220393	AY220393 Haematode
	30	11	100.0	166	8	AY220394	AY220394 Horsfield
	31	11	100.0	166	8	AY220395	AY220395 Iryanther
	32	11	100.0	167	8	AY220388	AY220388 Brochoneu
	33	11	100.0	167	8	AY220389	AY220389 Cephalosp
	34	11	100.0	167	8	AY220397	AY220397 Mauloutch
	35	11	100.0	169	8	AY220399	AY220399 Pycnanthu
	36	11	100.0	171	8	AY220400	AY220400 Virola mi
c	37	11	100.0	175	10	AF012184	AF012184 Mus muscu
	38	11	100.0	176	4	AF309694	AF309694 Megaptera
c	39	11	100.0	181	11	BV173634	BV173634 sqnm63498
	40	11	100.0	183	6	AR383946	AR383946 Sequence
	41	11	100.0	183	8	AY220384	AY220384 Cananga o
	42	11	100.0	190	8	AF117638S3	AF117640 Barclaya
	43	11	100.0	192	8	AY034303	AY034303 Lemna val
c	44	11	100.0	198	11	G02813	G02813 human STS W
c	45	11	100.0	198	11	G34422	G34422 human STS S

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 21:14:36 ; Search time 273 Seconds
(without alignments)
238.524 Million cell updates/sec

Title: US-10-070-587C-90
 Perfect score: 11
 Sequence: 1 tgaaatgctca 11

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query						
No.	Score	Match	Length	DB	ID		
c 1	11	100.0	11	4	AAS01923	Aas01923	Cytochrom
2	11	100.0	11	4	AAS01922	Aas01922	Cytochrom
3	11	100.0	19	3	AAC72719	Aac72719	Single nu
4	11	100.0	19	3	AAC72788	Aac72788	Single nu
c 5	11	100.0	20	6	ABK93614	Abk93614	Apoptotic
c 6	11	100.0	20	10	ABZ92227	Abz92227	Human oli
c 7	11	100.0	20	10	ABZ92228	Abz92228	Human oli
c 8	11	100.0	20	11	ABD28457	Abd28457	R78585-de
c 9	11	100.0	20	11	ABD28458	Abd28458	R78585-de
c 10	11	100.0	20	12	ADK95225	Adk95225	Primer of
c 11	11	100.0	20	12	ADQ14008	Adq14008	CAPN3/DYS
c 12	11	100.0	24	6	ABQ02402	Abq02402	Oligonucl
c 13	11	100.0	25	12	ADO11285	Ado11285	Single mu
c 14	11	100.0	27	12	ADJ46693	Adj46693	SNP TSC00

	15	11	100.0	28	12	ADJ46686	Adj46686 SNP TSC00
c	16	11	100.0	34	4	AAH91172	Aah91172 Human inf
c	17	11	100.0	60	6	ABN37062	Abn37062 Human spl
c	18	11	100.0	60	6	ABN47645	Abn47645 Human spl
	19	11	100.0	60	6	ABN45708	Abn45708 Human spl
	20	11	100.0	66	12	ADJ46688	Adj46688 SNP TSC00
	21	11	100.0	66	12	ADJ46689	Adj46689 SNP TSC00
	22	11	100.0	81	8	ABX55876	Abx55876 Bovine ES
	23	11	100.0	100	8	ACD68750	Acd68750 E. coli K
	24	11	100.0	100	8	ACD68751	Acd68751 E. coli K
	25	11	100.0	100	8	ACD68749	Acd68749 E. coli K
	26	11	100.0	104	10	ADB75954	Adb75954 Tomato pl
c	27	11	100.0	121	12	ADK91730	Adk91730 Polynucle
c	28	11	100.0	121	12	ADO13310	Ado13310 SNP targe
c	29	11	100.0	141	10	ABZ38913	Abz38913 N. gonorr
	30	11	100.0	143	8	ACA04722	Aca04722 cDNA enco
	31	11	100.0	146	10	ADJ81068	Adj81068 INSP010 n
c	32	11	100.0	150	8	ACA00902	Aca00902 C. glutam
	33	11	100.0	153	3	AAC13098	Aac13098 Human sec
c	34	11	100.0	182	8	ABX54604	Abx54604 Bovine ES
	35	11	100.0	183	11	ACH94880	Ach94880 Klebsiell
	36	11	100.0	192	12	ADJ46717	Adj46717 SNP TSC00
	37	11	100.0	199	3	AAC72721	Aac72721 Single nu
	38	11	100.0	199	3	AAC72790	Aac72790 Single nu
	39	11	100.0	204	2	AAT67344	Aat67344 H. pylori
	40	11	100.0	205	3	AAZ91625	Aaz91625 E.coli pr
	41	11	100.0	205	4	AAF55144	Aaf55144 Sulfometu
	42	11	100.0	207	4	AAL02475	Aal02475 Human rep
	43	11	100.0	209	3	AAC04696	Aac04696 Human sec
c	44	11	100.0	223	5	ABV59539	Abv59539 Human pro
c	45	11	100.0	224	12	ACH86796	Ach86796 Human gen

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 22:03:36 ; Search time 94 Seconds
(without alignments)
191.479 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 11
Sequence: 1 tgaaatgctca 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	11	100.0	20	3	US-09-690-364-61	Sequence 61, Appl
c	2	11	100.0	25	4	US-09-396-196G-71432	Sequence 71432, A
c	3	11	100.0	63	4	US-09-270-767-26425	Sequence 26425, A
	4	11	100.0	143	4	US-09-495-050A-170	Sequence 170, App
	5	11	100.0	153	4	US-09-513-999C-17173	Sequence 17173, A
	6	11	100.0	183	4	US-09-489-039A-675	Sequence 675, App
	7	11	100.0	205	3	US-08-735-545-12	Sequence 12, Appl
	8	11	100.0	205	3	US-09-449-083-12	Sequence 12, Appl
	9	11	100.0	209	4	US-09-513-999C-8771	Sequence 8771, Ap
	10	11	100.0	227	4	US-09-513-999C-30955	Sequence 30955, A
	11	11	100.0	263	4	US-09-513-999C-1838	Sequence 1838, Ap
	12	11	100.0	305	4	US-09-313-294A-533	Sequence 533, App
c	13	11	100.0	305	4	US-09-313-294A-533	Sequence 533, App
c	14	11	100.0	321	4	US-09-513-999C-33402	Sequence 33402, A
	15	11	100.0	343	4	US-09-265-585C-69	Sequence 69, Appl
c	16	11	100.0	346	4	US-09-621-976-10959	Sequence 10959, A
	17	11	100.0	357	4	US-09-513-999C-31668	Sequence 31668, A
c	18	11	100.0	375	4	US-09-513-999C-35833	Sequence 35833, A
	19	11	100.0	393	4	US-09-513-999C-1462	Sequence 1462, Ap
c	20	11	100.0	437	4	US-09-513-999C-13037	Sequence 13037, A
	21	11	100.0	449	4	US-09-270-767-26289	Sequence 26289, A
c	22	11	100.0	455	4	US-09-270-767-10935	Sequence 10935, A
c	23	11	100.0	456	4	US-09-328-352-2707	Sequence 2707, Ap
	24	11	100.0	466	4	US-09-621-976-15259	Sequence 15259, A
c	25	11	100.0	466	4	US-09-621-976-16107	Sequence 16107, A
c	26	11	100.0	495	4	US-09-621-976-8814	Sequence 8814, Ap
	27	11	100.0	514	4	US-09-684-938-156	Sequence 156, App
	28	11	100.0	514	4	US-09-308-825A-156	Sequence 156, App
	29	11	100.0	514	4	US-09-940-244-287	Sequence 287, App
c	30	11	100.0	516	4	US-09-621-976-2409	Sequence 2409, Ap
	31	11	100.0	521	3	US-09-404-879A-129	Sequence 129, App
	32	11	100.0	521	4	US-09-338-933-129	Sequence 129, App
	33	11	100.0	521	4	US-09-215-681-129	Sequence 129, App
	34	11	100.0	521	4	US-09-216-003A-129	Sequence 129, App

	35	11	100.0	521	4	US-09-667-857-129	Sequence 129, App
c	36	11	100.0	570	4	US-09-513-999C-3997	Sequence 3997, Ap
c	37	11	100.0	591	4	US-09-270-767-27913	Sequence 27913, A
	38	11	100.0	597	4	US-09-328-352-1138	Sequence 1138, Ap
	39	11	100.0	597	4	US-09-621-976-1303	Sequence 1303, Ap
c	40	11	100.0	598	3	US-08-998-416-368	Sequence 368, App
c	41	11	100.0	601	4	US-09-949-016-20229	Sequence 20229, A
	42	11	100.0	601	4	US-09-949-016-20928	Sequence 20928, A
	43	11	100.0	601	4	US-09-949-016-21830	Sequence 21830, A
	44	11	100.0	601	4	US-09-949-016-21831	Sequence 21831, A
	45	11	100.0	601	4	US-09-949-016-21832	Sequence 21832, A

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 22:18:47 ; Search time 312 Seconds
(without alignments)
216.459 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 11
Sequence: 1 tgaaatgctca 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	11	100.0	20	17	US-10-399-214-61						Sequence 61, Appl
	3	11	100.0	21	18	US-10-751-736-46854						Sequence 46854, A
	4	11	100.0	21	18	US-10-751-736-46857						Sequence 46857, A
	5	11	100.0	21	18	US-10-751-736-47877						Sequence 47877, A
	6	11	100.0	21	18	US-10-751-736-47880						Sequence 47880, A
c	7	11	100.0	24	10	US-09-940-185-2409						Sequence 2409, Ap
c	8	11	100.0	25	19	US-10-719-900-6437						Sequence 6437, Ap
c	9	11	100.0	25	19	US-10-719-900-6438						Sequence 6438, Ap
	10	11	100.0	25	19	US-10-719-900-99002						Sequence 99002, A
	11	11	100.0	25	19	US-10-719-900-147535						Sequence 147535,
c	12	11	100.0	25	19	US-10-719-900-255571						Sequence 255571,
c	13	11	100.0	25	19	US-10-719-900-255572						Sequence 255572,
c	14	11	100.0	25	19	US-10-719-900-295875						Sequence 295875,
c	15	11	100.0	25	19	US-10-719-900-329932						Sequence 329932,
	16	11	100.0	25	19	US-10-719-900-516534						Sequence 516534,
	17	11	100.0	25	19	US-10-719-900-516535						Sequence 516535,
	18	11	100.0	25	19	US-10-719-900-545653						Sequence 545653,
	19	11	100.0	25	19	US-10-719-900-635694						Sequence 635694,
c	20	11	100.0	25	19	US-10-719-900-711012						Sequence 711012,
c	21	11	100.0	25	19	US-10-719-900-780896						Sequence 780896,
c	22	11	100.0	25	19	US-10-719-900-839010						Sequence 839010,
	23	11	100.0	25	19	US-10-719-900-953670						Sequence 953670,
c	24	11	100.0	25	19	US-10-809-189-71432						Sequence 71432, A
c	25	11	100.0	60	10	US-09-908-975-9810						Sequence 9810, Ap
	26	11	100.0	60	10	US-09-908-975-18456						Sequence 18456, A
c	27	11	100.0	60	10	US-09-908-975-20393						Sequence 20393, A
	28	11	100.0	81	9	US-09-983-965-5805						Sequence 5805, Ap
	29	11	100.0	143	15	US-10-313-542-170						Sequence 170, App
	30	11	100.0	154	17	US-10-242-535A-47000						Sequence 47000, A
	31	11	100.0	154	17	US-10-085-783A-47000						Sequence 47000, A
	32	11	100.0	165	17	US-10-242-535A-15529						Sequence 15529, A
	33	11	100.0	165	17	US-10-085-783A-15529						Sequence 15529, A
c	34	11	100.0	182	9	US-09-983-965-4533						Sequence 4533, Ap
	35	11	100.0	182	18	US-10-425-115-25154						Sequence 25154, A
c	36	11	100.0	194	17	US-10-424-599-126314						Sequence 126314,
	37	11	100.0	201	18	US-10-741-601-5200						Sequence 5200, Ap
	38	11	100.0	201	18	US-10-741-601-5222						Sequence 5222, Ap

39	11	100.0	201	18	US-10-741-601-5245	Sequence 5245, Ap
40	11	100.0	201	18	US-10-741-601-5269	Sequence 5269, Ap
41	11	100.0	201	18	US-10-741-601-15524	Sequence 15524, A
42	11	100.0	201	18	US-10-741-601-20109	Sequence 20109, A
43	11	100.0	201	18	US-10-741-601-20161	Sequence 20161, A
c 44	11	100.0	201	18	US-10-741-601-22894	Sequence 22894, A
c 45	11	100.0	201	18	US-10-741-601-23258	Sequence 23258, A

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 21:34:11 ; Search time 1930 Seconds
(without alignments)
216.947 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 11
Sequence: 1 tgaaatgctca 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

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- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	11	100.0	72	8	AZ790292	AZ790292	2M0038C14
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c	3	11	100.0	74	8	BH809790	BH809790	SALK_0058
c	4	11	100.0	79	8	BZ584907	BZ584907	3590_1_61
c	5	11	100.0	87	6	CB227305	CB227305	1Ru37D09
c	6	11	100.0	87	6	CD946107	CD946107	REI_23 Ge
	7	11	100.0	87	6	CD952999	CD952999	SBF_27 Ge
c	8	11	100.0	93	8	AZ440614	AZ440614	1M0231G15
c	9	11	100.0	99	7	CF115774	CF115774	SSFP007N1
c	10	11	100.0	99	9	AJ594416	AJ594416	Arabidops
	11	11	100.0	103	7	CV367224	CV367224	PM2-BT076
	12	11	100.0	103	8	BH573680	BH573680	BOGFT27TF
	13	11	100.0	106	8	AZ895938	AZ895938	RPCI-24-2
c	14	11	100.0	107	5	BW327987	BW327987	BW327987
	15	11	100.0	107	7	CK832533	CK832533	4056060 B
c	16	11	100.0	108	6	CF030385	CF030385	QCD21d03.
	17	11	100.0	108	9	AL938072	AL938072	Arabidops
	18	11	100.0	110	8	AQ345309	AQ345309	RPCI11-12
c	19	11	100.0	114	7	CO912415	CO912415	BJ03032E0
c	20	11	100.0	118	1	AI638117	AI638117	ts50e10.x
	21	11	100.0	118	8	BH797563	BH797563	1008088F0
	22	11	100.0	119	2	AW493643	AW493643	UI-M-BH3-
c	23	11	100.0	119	9	BX532532	BX532532	Arabidops
c	24	11	100.0	122	6	CD162342	CD162342	ML1-0075T
c	25	11	100.0	122	9	CR395632	CR395632	Arabidops
c	26	11	100.0	123	8	BH007097	BH007097	ee63c12.x
	27	11	100.0	125	2	AW092267	AW092267	EST285447
c	28	11	100.0	127	2	BF289371	BF289371	EST453962
	29	11	100.0	128	4	BI051446	BI051446	CM4-GN033
	30	11	100.0	128	9	CG943227	CG943227	MBEEE95TF
c	31	11	100.0	129	2	AW757122	AW757122	sl29d07.y
	32	11	100.0	130	1	AL664576	AL664576	AL664576
	33	11	100.0	131	9	CG710446	CG710446	1119017D0
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	35	11	100.0	133	7	CF550632	CF550632	AGENCOURT
	36	11	100.0	134	7	CF333554	CF333554	JMT--02-I
c	37	11	100.0	134	9	BX944342	BX944342	Arabidops
	38	11	100.0	136	8	BH402913	BH402913	AG-ND-123
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c	40	11	100.0	137	5	BM878167	BM878167	if45h11.y
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	44	11	100.0	139	8	BZ138902	BZ138902	CH230-387
c	45	11	100.0	139	9	CG540684	CG540684	OST132928

US 6,025,131

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 22:03:36 ; Search time 94 Seconds
(without alignments)
191.479 Million cell updates/sec

Title: US-10-070-587C-90
Perfect score: 11
Sequence: 1 tgaaatgctca 11

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	11	100.0	25	4	US-09-396-196G-71432	Sequence 71432, A
c	3	11	100.0	63	4	US-09-270-767-26425	Sequence 26425, A
	4	11	100.0	143	4	US-09-495-050A-170	Sequence 170, App
	5	11	100.0	153	4	US-09-513-999C-17173	Sequence 17173, A
	6	11	100.0	183	4	US-09-489-039A-675	Sequence 675, App
	7	11	100.0	205	3	US-08-735-545-12	Sequence 12, Appl
	8	11	100.0	205	3	US-09-449-083-12	Sequence 12, Appl
	9	11	100.0	209	4	US-09-513-999C-8771	Sequence 8771, Ap

10	11	100.0	227	4	US-09-513-999C-30955	Sequence 30955, A
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c 14	11	100.0	321	4	US-09-513-999C-33402	Sequence 33402, A
15	11	100.0	343	4	US-09-265-585C-69	Sequence 69, Appl
c 16	11	100.0	346	4	US-09-621-976-10959	Sequence 10959, A
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c 18	11	100.0	375	4	US-09-513-999C-35833	Sequence 35833, A
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c 22	11	100.0	455	4	US-09-270-767-10935	Sequence 10935, A
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c 26	11	100.0	495	4	US-09-621-976-8814	Sequence 8814, Ap
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29	11	100.0	514	4	US-09-940-244-287	Sequence 287, App
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32	11	100.0	521	4	US-09-338-933-129	Sequence 129, App
33	11	100.0	521	4	US-09-215-681-129	Sequence 129, App
34	11	100.0	521	4	US-09-216-003A-129	Sequence 129, App
35	11	100.0	521	4	US-09-667-857-129	Sequence 129, App
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c 37	11	100.0	591	4	US-09-270-767-27913	Sequence 27913, A
38	11	100.0	597	4	US-09-328-352-1138	Sequence 1138, Ap
39	11	100.0	597	4	US-09-621-976-1303	Sequence 1303, Ap
c 40	11	100.0	598	3	US-08-998-416-368	Sequence 368, App
c 41	11	100.0	601	4	US-09-949-016-20229	Sequence 20229, A
42	11	100.0	601	4	US-09-949-016-20928	Sequence 20928, A
43	11	100.0	601	4	US-09-949-016-21830	Sequence 21830, A
44	11	100.0	601	4	US-09-949-016-21831	Sequence 21831, A
45	11	100.0	601	4	US-09-949-016-21832	Sequence 21832, A

ALIGNMENTS

RESULT 7

US-08-735-545-12

; Sequence 12, Application US/08735545

; Patent No. 6025131

; GENERAL INFORMATION:

; APPLICANT: Van Dyk, Tina K.

; APPLICANT: LaRossa, Robert Alan

; TITLE OF INVENTION: A Facile Method for

; TITLE OF INVENTION: Identifying Regulated

; TITLE OF INVENTION: Promoters

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS

```

;   ADDRESSEE:  AND COMPANY
;   STREET:    1007 MARKET STREET
;   CITY:     WILMINGTON
;   STATE:    DELAWARE
;   COUNTRY:  UNITED STATES OF AMERICA
;   ZIP:      19898
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  DISKETTE, 3.50 INCH
;   COMPUTER:    IBM PC COMPATIBLE
;   OPERATING SYSTEM:  MICROSOFT WINDOWS 3.1
;   SOFTWARE:    MICROSOFT WORD 2.0C
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/735,545
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:      FLOYD, LINDA A.
;   REGISTRATION NUMBER:  33,692
;   REFERENCE/DOCKET NUMBER:  CR-9989
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  302-892-8112
;   TELEFAX:    302-773-0164
;   INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:    205 base pairs
;   TYPE:      nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:   linear
;   MOLECULE TYPE:  DNA (genomic)
;   ORIGINAL SOURCE:
;   STRAIN:     dpd2089 lower
US-08-735-545-12

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Query Match          100.0%;  Score 11;  DB 3;  Length 205;
Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
Matches 11;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps
0;

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Qy          1 TGAAATGCTCA 11
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Db          134 TGAAATGCTCA 144

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